

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/669,656ADATE: 05/14/97
TIME: 08:26:21

INPUT SET: S17671.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Wood, John N.
6 Akopian, Armen N.
7
8 (ii) TITLE OF INVENTION: Ion Channel
9
10 (iii) NUMBER OF SEQUENCES: 31
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: ZENECA Pharmaceuticals
14 (B) STREET: 1800 Concord Pike, P.O. Box 15437
15 (C) CITY: Wilmington
16 (D) STATE: Delaware
17 (E) COUNTRY: USA
18 (F) ZIP: 19850
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: US 08/669,656
28 (B) FILING DATE: 24-JUN-1996
29 (C) CLASSIFICATION:
30
31 (viii) ATTORNEY/AGENT INFORMATION:
32 (A) NAME: Hohenschutz, Liza D.
33 (B) REGISTRATION NUMBER: 33,712
34 (C) REFERENCE/DOCKET NUMBER: PHM.70086
35
36 (ix) TELECOMMUNICATION INFORMATION:
37 (A) TELEPHONE: (302) 886-7466
38
39
40 (2) INFORMATION FOR SEQ ID NO:1:
41
42 (i) SEQUENCE CHARACTERISTICS:
43 (A) LENGTH: 6524 base pairs
44 (B) TYPE: nucleic acid
45 (C) STRANDEDNESS: single
46 (D) TOPOLOGY: linear

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47
48 (ii) MOLECULE TYPE: cDNA
49
50
51 (ix) FEATURE:
52 (A) NAME/KEY: CDS
53 (B) LOCATION: 204..6077
54
55
56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
57
58 TAGCTTGCTT CTGCTAATGC TACCCCAGGC CTTTAGACAG AGAACAGATG GCAGATGGAG 60
59
60 TTTCTTATTG CCATGCGCAA ACGCTGAGCC CACCTCATGA TCCCGGACCC CATGGTTTTTC 120
61
62 AGTAGACAAC CTGGGCTAAG AAGAGATCTC CGACCTTATA GAGCAGCAAA GAGTGTAAT 180
63
64 TCTTCCCCAA GAAGAATGAG AAG ATG GAG CTC CCC TTT GCG TCC GTG GGA 230
65 Met Glu Leu Pro Phe Ala Ser Val Gly
66 1 5
67
68 ACT ACC AAT TTC AGA CGG TTC ACT CCA GAG TCA CTG GCA GAG ATC GAG 278
69 Thr Thr Asn Phe Arg Arg Phe Thr Pro Glu Ser Leu Ala Glu Ile Glu
70 10 15 20 25
71
72 AAG CAG ATT GCT GCT CAC CGC GCA GCC AAG AAG GCC AGA ACC AAG CAC 326
73 Lys Gln Ile Ala Ala His Arg Ala Ala Lys Lys Ala Arg Thr Lys His
74 30 35 40
75
76 AGA GGA CAG GAG GAC AAG GGC GAG AAG CCC AGG CCT CAG CTG GAC TTG 374
77 Arg Gly Gln Glu Asp Lys Gly Glu Lys Pro Arg Pro Gln Leu Asp Leu
78 45 50 55
79
80 AAA GAC TGT AAC CAG CTG CCC AAG TTC TAT GGT GAG CTC CCA GCA GAA 422
81 Lys Asp Cys Asn Gln Leu Pro Lys Phe Tyr Gly Glu Leu Pro Ala Glu
82 60 65 70
83
84 CTG GTC GGG GAG CCC CTG GAG GAC CTA GAC CCT TTC TAC AGC ACA CAC 470
85 Leu Val Gly Glu Pro Leu Glu Asp Leu Asp Pro Phe Tyr Ser Thr His
86 75 80 85
87
88 CGG ACA TTC ATG GTG TTG AAT AAA AGC AGG ACC ATT TCC AGA TTC AGT 518
89 Arg Thr Phe Met Val Leu Asn Lys Ser Arg Thr Ile Ser Arg Phe Ser
90 90 95 100 105
91
92 GCC ACT TGG GCC CTG TGG CTC TTC AGT CCC TTC AAC CTG ATC AGA AGA 566
93 Ala Thr Trp Ala Leu Trp Leu Phe Ser Pro Phe Asn Leu Ile Arg Arg
94 110 115 120
95
96 ACA GCC ATC AAA GTG TCT GTC CAT TCC TGG TTC TCC ATA TTC ATC ACC 614
97 Thr Ala Ile Lys Val Ser Val His Ser Trp Phe Ser Ile Phe Ile Thr
98 125 130 135
99

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100	ATC	ACT	ATT	TTG	GTC	AAC	TGC	GTG	TGC	ATG	ACC	CGA	ACT	GAT	CTT	CCA	662
101	Ile	Thr	Ile	Leu	Val	Asn	Cys	Val	Cys	Met	Thr	Arg	Thr	Asp	Leu	Pro	
102			140					145					150				
103																	
104	GAG	AAA	GTC	GAG	TAC	GTC	TTC	ACT	GTC	ATT	TAC	ACC	TTC	GAG	GCT	CTG	710
105	Glu	Lys	Val	Glu	Tyr	Val	Phe	Thr	Val	Ile	Tyr	Thr	Phe	Glu	Ala	Leu	
106		155					160					165					
107																	
108	ATT	AAG	ATA	CTG	GCA	AGA	GGG	TTT	TGT	CTA	AAT	GAG	TTC	ACT	TAT	CTT	758
109	Ile	Lys	Ile	Leu	Ala	Arg	Gly	Phe	Cys	Leu	Asn	Glu	Phe	Thr	Tyr	Leu	
110	170					175				180						185	
111																	
112	CGA	GAT	CCG	TGG	AAC	TGG	CTG	GAC	TTC	AGT	GTC	ATT	ACC	TTG	GCG	TAT	806
113	Arg	Asp	Pro	Trp	Asn	Trp	Leu	Asp	Phe	Ser	Val	Ile	Thr	Leu	Ala	Tyr	
114					190					195					200		
115																	
116	GTG	GGT	GCA	GCG	ATA	GAC	CTC	CGA	GGA	ATC	TCA	GGC	CTG	CGG	ACA	TTC	854
117	Val	Gly	Ala	Ala	Ile	Asp	Leu	Arg	Gly	Ile	Ser	Gly	Leu	Arg	Thr	Phe	
118				205					210				215				
119																	
120	CGA	GTT	CTC	AGA	GCC	CTG	AAA	ACT	GTT	TCT	GTG	ATC	CCA	GGA	CTG	AAG	902
121	Arg	Val	Leu	Arg	Ala	Leu	Lys	Thr	Val	Ser	Val	Ile	Pro	Gly	Leu	Lys	
122			220					225					230				
123																	
124	GTC	ATC	GTG	GGA	GCC	CTG	ATC	CAC	TCA	GTG	AGG	AAG	CTG	GCC	GAC	GTG	950
125	Val	Ile	Val	Gly	Ala	Leu	Ile	His	Ser	Val	Arg	Lys	Leu	Ala	Asp	Val	
126		235					240					245					
127																	
128	ACT	ATC	CTC	ACA	GTC	TTC	TGC	CTG	AGC	GTC	TTC	GCC	TTG	GTG	GGC	CTG	998
129	Thr	Ile	Leu	Thr	Val	Phe	Cys	Leu	Ser	Val	Phe	Ala	Leu	Val	Gly	Leu	
130	250					255					260				265		
131																	
132	CAG	CTC	TTT	AAG	GGG	AAC	CTT	AAG	AAC	AAA	TGC	ATC	AGG	AAC	GGA	ACA	1046
133	Gln	Leu	Phe	Lys	Gly	Asn	Leu	Lys	Asn	Lys	Cys	Ile	Arg	Asn	Gly	Thr	
134					270					275					280		
135																	
136	GAT	CCC	CAC	AAG	GCT	GAC	AAC	CTC	TCA	TCT	GAA	ATG	GCA	GAA	TAC	GTC	1094
137	Asp	Pro	His	Lys	Ala	Asp	Asn	Leu	Ser	Ser	Glu	Met	Ala	Glu	Tyr	Val	
138				285					290				295				
139																	
140	TCC	ATC	AAG	CCT	GGT	ACT	ACG	GAT	CCC	TTA	CTG	TGC	GGC	AAT	GGG	TCT	1142
141	Ser	Ile	Lys	Pro	Gly	Thr	Thr	Asp	Pro	Leu	Leu	Cys	Gly	Asn	Gly	Ser	
142			300					305					310				
143																	
144	GAT	GCT	GGT	CAC	TGC	CCT	GGA	GGC	TAT	GTC	TGC	CTG	AAA	ACT	CCT	GAC	1190
145	Asp	Ala	Gly	His	Cys	Pro	Gly	Gly	Tyr	Val	Cys	Leu	Lys	Thr	Pro	Asp	
146		315					320					325					
147																	
148	AAC	CCG	GAT	TTT	AAC	TAC	ACC	AGC	TTT	GAT	TCC	TTT	GCG	TGG	GCA	TTC	1238
149	Asn	Pro	Asp	Phe	Asn	Tyr	Thr	Ser	Phe	Asp	Ser	Phe	Ala	Trp	Ala	Phe	
150	330					335					340				345		
151																	
152	CTC	TCA	CTG	TTC	CGC	CTC	ATG	ACG	CAG	GAC	TCC	TGG	GAG	CGC	CTG	TAC	1286

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153	Leu Ser Leu Phe Arg Leu Met Thr Gln Asp Ser Trp Glu Arg Leu Tyr	
154	350 355 360	
155		
156	CAG CAG ACA CTC CGG GCT TCT GGG AAA ATG TAC ATG GTC TTT TTC GTG	1334
157	Gln Gln Thr Leu Arg Ala Ser Gly Lys Met Tyr Met Val Phe Phe Val	
158	365 370 375	
159		
160	CTG GTT ATT TTC CTT GGA TCG TTC TAC CTG GTC AAT TTG ATC TTG GCC	1382
161	Leu Val Ile Phe Leu Gly Ser Phe Tyr Leu Val Asn Leu Ile Leu Ala	
162	380 385 390	
163		
164	GTG GTC ACC ATG GCG TAT GAA GAG CAG AGC CAG GCA ACA ATT GCA GAA	1430
165	Val Val Thr Met Ala Tyr Glu Glu Gln Ser Gln Ala Thr Ile Ala Glu	
166	395 400 405	
167		
168	ATC GAA GCC AAG GAA AAA AAG TTC CAG GAA GCC CTT GAG GTG CTG CAG	1478
169	Ile Glu Ala Lys Glu Lys Lys Phe Gln Glu Ala Leu Glu Val Leu Gln	
170	410 415 420 425	
171		
172	AAG GAA CAG GAG GTG CTG GCA GCC CTG GGG ATT GAC ACG ACC TCG CTC	1526
173	Lys Glu Gln Glu Val Leu Ala Ala Leu Gly Ile Asp Thr Thr Ser Leu	
174	430 435 440	
175		
176	CAG TCC CAC AGT GGA TCA CCC TTA GCC TCC AAA AAC GCC AAT GAG AGA	1574
177	Gln Ser His Ser Gly Ser Pro Leu Ala Ser Lys Asn Ala Asn Glu Arg	
178	445 450 455	
179		
180	AGA CCC AGG GTG AAA TCA AGG GTG TCA GAG GGC TCC ACG GAT GAC AAC	1622
181	Arg Pro Arg Val Lys Ser Arg Val Ser Glu Gly Ser Thr Asp Asp Asn	
182	460 465 470	
183		
184	AGG TCA CCC CAA TCT GAC CCT TAC AAC CAG CGC AGG ATG TCT TTC CTA	1670
185	Arg Ser Pro Gln Ser Asp Pro Tyr Asn Gln Arg Arg Met Ser Phe Leu	
186	475 480 485	
187		
188	GGC CTG TCT TCA GGA AGA CGC AGG GCT AGC CAC GGC AGT GTG TTC CAC	1718
189	Gly Leu Ser Ser Gly Arg Arg Arg Ala Ser His Gly Ser Val Phe His	
190	490 495 500 505	
191		
192	TTC CGA GCG CCC AGC CAA GAC ATC TCA TTT CCT GAC GGG ATC ACC CCT	1766
193	Phe Arg Ala Pro Ser Gln Asp Ile Ser Phe Pro Asp Gly Ile Thr Pro	
194	510 515 520	
195		
196	GAT GAT GGG GTC TTT CAC GGA GAC CAG GAA AGC CGT CGA GGT TCC ATA	1814
197	Asp Asp Gly Val Phe His Gly Asp Gln Glu Ser Arg Arg Gly Ser Ile	
198	525 530 535	
199		
200	TTG CTG GGC AGG GGT GCT GGG CAG ACA GGT CCA CTC CCC AGG AGC CCA	1862
201	Leu Leu Gly Arg Gly Ala Gly Gln Thr Gly Pro Leu Pro Arg Ser Pro	
202	540 545 550	
203		
204	CTG CCT CAG TCC CCC AAC CCT GGC CGT AGA CAT GGA GAA GAG GGA CAG	1910
205	Leu Pro Gln Ser Pro Asn Pro Gly Arg Arg His Gly Glu Glu Gly Gln	

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206	555	560	565	
207				
208	CTC GGA GTG CCC ACT GGT GAG CTT ACC GCT GGA GCG CCT GAA GGC CCG			1958
209	Leu Gly Val Pro Thr Gly Glu Leu Thr Ala Gly Ala Pro Glu Gly Pro			
210	570	575	580	585
211				
212	GCA CTG CAC ACT ACA GGG CAG AAG AGC TTC CTG TCT GCG GGC TAC TTG			2006
213	Ala Leu His Thr Thr Gly Gln Lys Ser Phe Leu Ser Ala Gly Tyr Leu			
214		590	595	600
215				
216	AAC GAA CCT TTC CGA GCA CAG AGG GCC ATG AGC GTT GTC AGT ATC ATG			2054
217	Asn Glu Pro Phe Arg Ala Gln Arg Ala Met Ser Val Val Ser Ile Met			
218		605	610	615
219				
220	ACT TCT GTC ATT GAG GAG CTT GAA GAG TCT AAG CTG AAG TGC CCA CCC			2102
221	Thr Ser Val Ile Glu Glu Leu Glu Glu Ser Lys Leu Lys Cys Pro Pro			
222		620	625	630
223				
224	TGC TTG ATC AGC TTC GCT CAG AAG TAT CTG ATC TGG GAG TGC TGC CCC			2150
225	Cys Leu Ile Ser Phe Ala Gln Lys Tyr Leu Ile Trp Glu Cys Cys Pro			
226		635	640	645
227				
228	AAG TGG AGG AAG TTC AAG ATG GCG CTG TTC GAG CTG GTG ACT GAC CCC			2198
229	Lys Trp Arg Lys Phe Lys Met Ala Leu Phe Glu Leu Val Thr Asp Pro			
230		650	655	660
231				665
232	TTC GCA GAG CTT ACC ATC ACC CTC TGC ATC GTG GTG AAC ACC GTC TTC			2246
233	Phe Ala Glu Leu Thr Ile Thr Leu Cys Ile Val Val Asn Thr Val Phe			
234		670	675	680
235				
236	ATG GCC ATG GAG CAC TAC CCC ATG ACC GAT GCC TTC GAT GCC ATG CTT			2294
237	Met Ala Met Glu His Tyr Pro Met Thr Asp Ala Phe Asp Ala Met Leu			
238		685	690	695
239				
240	CAA GCC GGC AAC ATT GTC TTC ACC GTG TTT TTC ACA ATG GAG ATG GCC			2342
241	Gln Ala Gly Asn Ile Val Phe Thr Val Phe Phe Thr Met Glu Met Ala			
242		700	705	710
243				
244	TTC AAG ATC ATT GCC TTC GAC CCC TAC TAT TAC TTC CAG AAG AAG TGG			2390
245	Phe Lys Ile Ile Ala Phe Asp Pro Tyr Tyr Tyr Phe Gln Lys Lys Trp			
246		715	720	725
247				
248	AAT ATC TTC GAC TGT GTC ATC GTC ACC GTG AGC CTT CTG GAG CTG AGT			2438
249	Asn Ile Phe Asp Cys Val Ile Val Thr Val Ser Leu Leu Glu Leu Ser			
250		730	735	740
251				745
252	GCA TCC AAG AAG GGC AGC CTG TCT GTG CTC CGT ACC TTA CGC TTG CTG			2486
253	Ala Ser Lys Lys Gly Ser Leu Ser Val Leu Arg Thr Leu Arg Leu Leu			
254		750	755	760
255				
256	CGG GTC TTC AAG CTG GCC AAG TCC TGG CCC ACC CTG AAC ACC CTC ATC			2534
257	Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu Asn Thr Leu Ile			
258		765	770	775

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SEQUENCE VERIFICATION REPORT
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Original Text